



SEQUENCE LISTING

PHa
CHW
8-6-99

(1) GENERAL INFORMATION:

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- (i) APPLICANT: Lester, Henry A.
Davidson, Norman
Kofuji, Paulo

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- (ii) TITLE OF INVENTION: INWARD RECTIFIER, G-PROTEIN ACTIVATED,
MAMMALIAN, POTASSIUM CHANNELS AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 2

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- (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
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(C) CITY: San Francisco
(D) STATE: California

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- (E) COUNTRY: United States
(F) ZIP: 94111-4187

- (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

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- (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 09/039,927
(B) FILING DATE: 16-MAR-1998
(C) CLASSIFICATION:

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- (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/066,371
(B) FILING DATE: 21-MAR-1993

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- (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Trecartin, Richard F.
(B) REGISTRATION NUMBER: 31,801
(C) REFERENCE/DOCKET NUMBER: A-63098-1/RFT

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- (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (415) 781-1989
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(C) TELEX: 910 277299

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(2) INFORMATION FOR SEQ ID NO:1:

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- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2076 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: cDNA

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- (ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 32..1534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGAA	TCTGGATCTC	CCCTCCGTAT	T	ATG TCT GCA CTC CGA AGG AAA	52
				Met Ser Ala Leu Arg Arg Lys	
5			1	5	
TTT GGG GAC GAT TAC CAG GTA GTG ACC ACT TCG TCC AGC GGT TCG GGC	Phe Gly Asp Asp Tyr Gln Val Val Thr Thr Ser Ser Gly Ser Gly	10	15	20	100
TTG CAG CCC CAG GGG CCA GGA CAG GGC CCA CAG CAG CAG CTT GTA CCC	Leu Gln Pro Gln Gly Pro Gln Gly Pro Gln Gln Gln Leu Val Pro	10	25	30	148
AAG AAG AAA CGG CAG CGG TTC GTG GAC AAG AAC GGT CGG TGC AAT GTG	Lys Lys Arg Gln Arg Phe Val Asp Lys Asn Gly Arg Cys Asn Val	15	40	45	196
CAG CAC GGC AAC CTG GGC AGC GAG ACC AGT CGC TAC CTT TCC GAC CTC	Gln His Gly Asn Leu Gly Ser Glu Thr Ser Arg Tyr Leu Ser Asp Leu	20	60	65	244
TTC ACT ACC CTG GTG GAT CTC AAG TGG CGT TGG AAC CTC TTT ATC TTC	Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Trp Asn Leu Phe Ile Phe	25	75	80	292
ATC CTC ACC TAC ACC GTG GCC TGG CTC TTC ATG GCG TCC ATG TGG TGG	Ile Leu Thr Tyr Thr Val Ala Trp Leu Phe Met Ala Ser Met Trp Trp	30	90	95	340
GTG ATC GCT TAT ACC CGG GGC GAC CTG AAC AAA GCC CAT GTC GGC AAC	Val Ile Ala Tyr Thr Arg Gly Asp Leu Asn Lys Ala His Val Gly Asn	35	105	110	388
TAC ACT CCC TGT GTG GCC AAT GTC TAT AAC TTC CCC TCT GCC TTC CTT	Tyr Thr Pro Cys Val Ala Asn Val Tyr Asn Phe Pro Ser Ala Phe Leu	40	120	125	436
TTC TTC ATC GAG ACC GAG GCC ACC ATC GGC TAT GGC TAC CGC TAC ATC	Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly Tyr Gly Tyr Arg Tyr Ile	45	140	145	484
ACC GAC AAG TGC CCC GAG GGC ATC ATC CTT TTC CTT TTC CAG TCC ATC	Thr Asp Lys Cys Pro Glu Gly Ile Ile Leu Phe Leu Phe Gln Ser Ile	50	155	160	532
CTT GGC TCC ATC GTG GAC GCT TTC CTC ATC GGC TGC ATG TTC ATC AAG	Leu Gly Ser Ile Val Asp Ala Phe Leu Ile Gly Cys Met Phe Ile Lys	55	170	175	580
ATG TCC CAG CCC AAA AAG CGC GCC GAG ACC CTC ATG TTT AGC GAG CAT	Met Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Met Phe Ser Glu His	60	185	190	628
GCG GTT ATT TCC ATG AGG GAC GGA AAA CTC ACT CTC ATG TTC CGG GTG	Ala Val Ile Ser Met Arg Asp Gly Lys Leu Thr Leu Met Phe Arg Val	65	200	205	676
GGC AAC CTG CGC AAC AGC CAC ATG GTC TCC GCG CAG ATC CGC TGC AAG	Gly Asn Leu Arg Asn Ser His Met Val Ser Ala Gln Ile Arg Cys Lys	70	220	225	724
CTG CTC AAA TCT CGG CAG ACA CCT GAG GGT GAG TTT CTA CCC CTT GAC	Leu Leu Lys Ser Arg Gln Thr Pro Glu Gly Glu Phe Leu Pro Leu Asp	75	235	240	772
				245	

	CAA CTT GAA CTG GAT GTA GGT TTT AGT ACA GGG GCA GAT CAA CTT TTT	820
	Gln Leu Glu Leu Asp Val Gly Phe Ser Thr Gly Ala Asp Gln Leu Phe	
	250 255 260	
5	CTT GTG TCC CCT CTC ACC ATT TGC CAC GTG ATC GAT GCC AAA AGC CCC	868
	Leu Val Ser Pro Leu Thr Ile Cys His Val Ile Asp Ala Lys Ser Pro	
	265 270 275	
10	TTT TAT GAC CTA TCC CAG CGA AGC ATG CAA ACT GAA CAG TTC GAG GTG	916
	Phe Tyr Asp Leu Ser Gln Arg Ser Met Gln Thr Glu Gln Phe Glu Val	
	280 285 290 295	
15	GTC GTC ATC CTG GAA GGC ATC GTG GAA ACC ACA GGG ATG ACT TGT CAA	964
	Val Val Ile Leu Glu Gly Ile Val Glu Thr Thr Gly Met Thr Cys Gln	
	300 305 310	
	GCT CGA ACA TCA TAC ACC GAA GAT GAA GTT CTT TGG GGT CAT CGT TTT	1012
	Ala Arg Thr Ser Tyr Thr Glu Asp Glu Val Leu Trp Gly His Arg Phe	
	315 320 325	
20	TTC CCT GTA ATT TCT TTA GAA GAA GGA TTC TTT AAA GTC GAT TAC TCC	1060
	Phe Pro Val Ile Ser Leu Glu Glu Gly Phe Phe Lys Val Asp Tyr Ser	
	330 335 340	
25	CAG TTC CAT GCA ACC TTT GAA GTC CCC ACC CCT CCG TAC AGT GTG AAA	1108
	Gln Phe His Ala Thr Phe Glu Val Pro Thr Pro Tyr Ser Val Lys	
	345 350 355	
30	GAG CAG GAA GAA ATG CTT CTC ATG TCT TCC CCT TTA ATA GCA CCA GCC	1156
	Glu Gln Glu Glu Met Leu Leu Met Ser Ser Pro Leu Ile Ala Pro Ala	
	360 365 370 375	
35	ATA ACC AAC AGC AAA GAA AGA CAC AAT TCT GTG GAG TGC TTA GAT GGA	1204
	Ile Thr Asn Ser Lys Glu Arg His Asn Ser Val Glu Cys Leu Asp Gly	
	380 385 390	
	CTA GAT GAC ATT AGC ACA AAA CTT CCA TCG AAG CTG CAG AAA ATT ACG	1252
	Leu Asp Asp Ile Ser Thr Lys Leu Pro Ser Lys Leu Gln Lys Ile Thr	
	395 400 405	
40	GGG AGA GAA GAC TTT CCC AAA AAA CTC CTG AGG ATG AGT TCT ACA ACT	1300
	Gly Arg Glu Asp Phe Pro Lys Lys Leu Leu Arg Met Ser Ser Thr Thr	
	410 415 420	
45	TCA GAA AAA GCC TAT AGT TTG GGT GAT TTG CCC ATG AAA CTC CAA CGA	1348
	Ser Glu Lys Ala Tyr Ser Leu Gly Asp Leu Pro Met Lys Leu Gln Arg	
	425 430 435	
50	ATA AGT TCG GTT CCT GGC AAC TCT GAA GAA AAA CTG GTA TCT AAA ACC	1396
	Ile Ser Ser Val Pro Gly Asn Ser Glu Glu Lys Leu Val Ser Lys Thr	
	440 445 450 455	
55	ACC AAG ATG TTA TCA GAT CCC ATG AGC CAG TCT GTG GCC GAT TTG CCA	1444
	Thr Lys Met Leu Ser Asp Pro Met Ser Gln Ser Val Ala Asp Leu Pro	
	460 465 470	
	CCG AAG CTT CAA AAG ATG GCT GGA GGA CCT ACC AGG ATG GAA GGG AAT	1492
	Pro Lys Leu Gln Lys Met Ala Gly Gly Pro Thr Arg Met Glu Gly Asn	
	475 480 485	
60	CTT CCA GCC AAA CTA AGA AAA ATG AAC TCT GAC CGC TTC ACA	1534
	Leu Pro Ala Lys Leu Arg Lys Met Asn Ser Asp Arg Phe Thr	
	490 495 500	
65	TAGCAAAACA CCCCCATTAGG CATTATTTCA TGTTTGATT TAGTTTAGT CCAATATTTG	1594
	GCTGATAAGA TAATCCTCCC CGGGAAATCT GAGAGGTCTA TCCCAGTCTG GCAAATTCAT	
	1654	

	CAGAGGACTC TTCATTGAAG TGTTGTTACT GTGTTGAACA TGAGTTACAA AGGGAGGACA	1714
	TCATAAGAAA GCTAATAGTT GGCGATGTATT ATCACACATCAA GCATGCAATA ATGTGCAAAT	1774
5	TTTGCATTTA GTTTCTGGC ATGATTATA TATGGCATAT TTATATTGAA TATTCTGGAA	1834
	AAATATATAA ATATATATTT GAAGTGGAGA TATTCTCCCC ATAATTCTA ATATATGTAT	1894
	TAAGCCAAAC ATGAGTGGAT AGCTTCAGG GCACTAAAAT AATATACATG CATAACATACA	1954
10	TACATGCATA TGCACAGACA CATAACACACA CATAACTCATA TATATAAAAC ATACCCATAC	2014
	AAACATATAT ATCTAATAAA AATTGTGATG TTTTGTCAA AAAAAAAAAA AAAAAAACTCG	2074
15	AG	2076

(2) INFORMATION FOR SEQ ID NO:2:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 501 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

30	Met	Ser	Ala	Leu	Arg	Arg	Lys	Phe	Gly	Asp	Asp	Tyr	Gln	Val	Val	Thr
	1			5					10				15			

Thr Ser Ser Ser Gly Ser Gly Leu Gln Pro Gln Gly Pro Gly Gln Gly
20 25 30

35 Pro Gln Gln Gln Leu Val Pro Lys Lys Lys Arg Gln Arg Phe Val Asp
35 40 45

Lys Asn Gly Arg Cys Asn Val Gln His Gly Asn Leu Gly Ser Glu Thr
50 55 60

40 Ser Arg Tyr Leu Ser Asp Leu Phe Thr Thr Leu Val Asp Leu Lys Trp
65 70 75 80

Arg Trp Asn Leu Phe Ile Phe Ile Leu Thr Tyr Thr Val Ala Trp Leu
 85 90 95

Phe Met Ala Ser Met Trp Trp Val Ile Ala Tyr Thr Arg Gly Asp Leu
 100 105 110
 50 Asn Lys Ala His Val Gly Asn Tyr Thr Pro Cys Val Ala Asn Val Tyr

Asn Phe Pro Ser Ala Phe Leu Phe Phe Ile Glu Thr Glu Ala Thr Ile

Gly Tyr Gly Tyr Arg Tyr Ile Thr Asp Lys Cys Pro Glu Gly Ile Ile

60 Leu Phe Leu Phe Gln Ser Ile Leu Gly Ser Ile Val Asp Ala Phe Leu
165 170 175

Ile Gly Cys Met Phe Ile Lys Met Ser Gln Pro Lys Lys Arg Ala Glu
100 105 110

65 180 185 190
 Thr Leu Met Phe Ser Glu His Ala Val Ile Ser Met Arg Asp Gly Lys
 185 200 205

Leu Thr Leu Met Phe Arg Val Gly Asn Leu Arg Asn Ser His Met Val
210 215 220

5 Ser Ala Gln Ile Arg Cys Lys Leu Leu Lys Ser Arg Gln Thr Pro Glu
225 230 235 240

Gly Glu Phe Leu Pro Leu Asp Gln Leu Glu Leu Asp Val Gly Phe Ser
245 250 255

10 Thr Gly Ala Asp Gln Leu Phe Leu Val Ser Pro Leu Thr Ile Cys His
260 265 270

Val Ile Asp Ala Lys Ser Pro Phe Tyr Asp Leu Ser Gln Arg Ser Met
275 280 285

15 Gln Thr Glu Gln Phe Glu Val Val Val Ile Leu Glu Gly Ile Val Glu
290 295 300

Thr Thr Gly Met Thr Cys Gln Ala Arg Thr Ser Tyr Thr Glu Asp Glu
20 305 310 315 320

Val Leu Trp Gly His Arg Phe Phe Pro Val Ile Ser Leu Glu Glu Gly
325 330 335

25 Phe Phe Lys Val Asp Tyr Ser Gln Phe His Ala Thr Phe Glu Val Pro
340 345 350

Thr Pro Pro Tyr Ser Val Lys Glu Gln Glu Glu Met Leu Leu Met Ser
355 360 365

30 Ser Pro Leu Ile Ala Pro Ala Ile Thr Asn Ser Lys Glu Arg His Asn
370 375 380

Ser Val Glu Cys Leu Asp Gly Leu Asp Asp Ile Ser Thr Lys Leu Pro
385 390 395 400

Ser Lys Leu Gln Lys Ile Thr Gly Arg Glu Asp Phe Pro Lys Lys Leu
405 410 415

40 Leu Arg Met Ser Ser Thr Thr Ser Glu Lys Ala Tyr Ser Leu Gly Asp
420 425 430

Leu Pro Met Lys Leu Gln Arg Ile Ser Ser Val Pro Gly Asn Ser Glu
435 440 445

45 Glu Lys Leu Val Ser Lys Thr Thr Lys Met Leu Ser Asp Pro Met Ser
450 455 460

Gln Ser Val Ala Asp Leu Pro Pro Lys Leu Gln Lys Met Ala Gly Gly
50 465 470 475 480

Pro Thr Arg Met Glu Gly Asn Leu Pro Ala Lys Leu Arg Lys Met Asn
485 490 495

55 Ser Asp Arg Phe Thr
500